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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/879,257A

DATE: 10/23/2001

TIME: 09:56:25

#5

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Output Set: N:\CRF3\10232001\I879257A.raw

3 <110> APPLICANT: YAMAMOTO, SACHIKO
4 HANADA, TOSHIRO
5 SHIRO, MINORU
6 KOBATAKE, SHINZO
8 <120> TITLE OF INVENTION: HYBRID ENZYMES AND USE THEREOF *ck*
10 <130> FILE REFERENCE: 55986(70281)
12 <140> CURRENT APPLICATION NUMBER: 09/879,257A
13 <141> CURRENT FILING DATE: 2001-06-12
15 <160> NUMBER OF SEQ ID NOS: 56
17 <170> SOFTWARE: PatentIn Ver. 2.1
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 206
21 <212> TYPE: PRT
22 <213> ORGANISM: Homo sapiens
24 <400> SEQUENCE: 1
25 Gln Thr Asp Met Ser Arg Lys Ala Phe Val Phe Pro Lys Glu Ser Asp
26 1 5 10 15
28 Thr Ser Tyr Val Ser Leu Lys Ala Pro Leu Thr Lys Pro Leu Lys Ala
29 20 25 30
31 Phe Thr Val Cys Leu His Phe Tyr Thr Glu Leu Ser Ser Thr Arg Gly
32 35 40 45
34 Tyr Ser Ile Phe Ser Tyr Ala Thr Lys Arg Gln Asp Asn Glu Ile Leu
35 50 55 60
37 Ile Phe Trp Ser Lys Asp Ile Gly Tyr Ser Phe Thr Val Gly Gly Ser
38 65 70 75 80
40 Glu Ile Leu Phe Glu Val Pro Glu Val Thr Val Ala Pro Val His Ile
41 85 90 95
43 Cys Thr Ser Trp Glu Ser Ala Ser Gly Ile Val Glu Phe Trp Val Asp
44 100 105 110
46 Gly Lys Pro Arg Val Arg Lys Ser Leu Lys Lys Gly Tyr Thr Val Gly
47 115 120 125
49 Ala Glu Ala Ser Ile Ile Leu Gly Gln Glu Gln Asp Ser Phe Gly Gly
50 130 135 140
52 Asn Phe Glu Gly Ser Gln Ser Leu Val Gly Asp Ile Gly Asn Val Asn
53 145 150 155 160
55 Met Trp Asp Phe Val Leu Ser Pro Asp Glu Ile Asn Thr Ile Tyr Leu
56 165 170 175
58 Gly Gly Pro Phe Ser Pro Asn Val Leu Asn Trp Arg Ala Leu Lys Tyr
59 180 185 190
61 Glu Val Gln Gly Glu Val Phe Thr Lys Pro Gln Leu Trp Pro
62 195 200 205
65 <210> SEQ ID NO: 2
66 <211> LENGTH: 16
67 <212> TYPE: PRT
68 <213> ORGANISM: Homo sapiens
70 <400> SEQUENCE: 2
71 Asp Met Ser Arg Lys Ala Phe Val Phe Pro Lys Glu Ser Asp Thr Ser

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72      1              5              10              15
75 <210> SEQ ID NO: 3
76 <211> LENGTH: 27
77 <212> TYPE: PRT
78 <213> ORGANISM: Homo sapiens
80 <400> SEQUENCE: 3
81 Leu Val Gly Asp Ile Gly Asn Val Asn Met Trp Asp Phe Val Leu Ser
82      1              5              10              15
84 Pro Asp Glu Ile Asn Thr Ile Tyr Leu Gly Gly
85      20              25
88 <210> SEQ ID NO: 4
89 <211> LENGTH: 12
90 <212> TYPE: PRT
91 <213> ORGANISM: Homo sapiens
93 <400> SEQUENCE: 4
94 Leu Lys Lys Gly Tyr Thr Val Gly Ala Glu Ala Ser
95      1              5              10
98 <210> SEQ ID NO: 5
99 <211> LENGTH: 10
100 <212> TYPE: PRT
101 <213> ORGANISM: Homo sapiens
103 <400> SEQUENCE: 5
104 Arg Ala Leu Lys Tyr Glu Val Gln Gly Glu
105      1              5              10
108 <210> SEQ ID NO: 6
109 <211> LENGTH: 486
110 <212> TYPE: PRT
111 <213> ORGANISM: Leuconostoc mesenteroides
113 <400> SEQUENCE: 6
114 Met Val Ser Glu Ile Lys Thr Leu Val Thr Phe Phe Gly Gly Thr Gly
115      1              5              10              15
117 Asp Leu Ala Lys Arg Lys Leu Tyr Pro Ser Val Phe Asn Leu Tyr Lys
118      20              25              30
120 Lys Gly Tyr Leu Gln Lys His Phe Ala Ile Val Gly Thr Ala Arg Gln
121      35              40              45
123 Ala Leu Asn Asp Asp Glu Phe Lys Gln Leu Val Arg Asp Ser Ile Lys
124      50              55              60
126 Asp Phe Thr Asp Asp Gln Ala Gln Ala Glu Ala Phe Ile Glu His Phe
127      65              70              75              80
129 Ser Tyr Arg Ala His Asp Val Thr Asp Ala Ala Ser Tyr Ala Val Leu
130      85              90              95
132 Lys Glu Ala Ile Glu Glu Ala Ala Asp Lys Phe Asp Ile Asp Gly Asn
133      100             105             110
135 Arg Ile Phe Tyr Met Ser Val Ala Pro Arg Phe Phe Gly Thr Ile Ala
136      115             120             125
138 Lys Tyr Leu Lys Ser Glu Gly Leu Leu Ala Asp Thr Gly Tyr Asn Arg
139      130             135             140
141 Leu Met Ile Glu Lys Pro Phe Gly Thr Ser Tyr Asp Thr Ala Ala Glu
142 145             150             155             160

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144 Leu Gln Asn Asp Leu Glu Asn Ala Phe Asp Asp Asn Gln Leu Phe Arg
145                               165                               170                               175
147 Ile Asp His Tyr Leu Gly Lys Glu Met Val Gln Asn Ile Ala Ala Leu
148                               180                               185                               190
150 Arg Phe Gly Asn Pro Ile Phe Asp Ala Ala Trp Asn Lys Asp Tyr Ile
151                               195                               200                               205
153 Lys Asn Val Gln Val Thr Leu Ser Glu Val Leu Gly Val Glu Glu Arg
154                               210                               215                               220
156 Ala Gly Tyr Tyr Asp Thr Ala Gly Ala Leu Leu Asp Met Ile Gln Asn
157 225                               230                               235                               240
159 His Thr Met Gln Ile Val Gly Trp Leu Ala Met Glu Lys Pro Glu Ser
160                               245                               250                               255
162 Phe Thr Asp Lys Asp Ile Arg Ala Ala Lys Asn Ala Ala Phe Asn Ala
163                               260                               265                               270
165 Leu Lys Ile Tyr Asp Glu Ala Glu Val Asn Lys Tyr Phe Val Arg Ala
166                               275                               280                               285
168 Gln Tyr Gly Ala Gly Asp Ser Ala Asp Phe Lys Pro Tyr Leu Glu Glu
169                               290                               295                               300
171 Leu Asp Val Pro Ala Asp Ser Lys Asn Asn Thr Phe Ile Ala Gly Glu
172 305                               310                               315                               320
174 Leu Gln Phe Asp Leu Pro Arg Trp Glu Gly Val Pro Phe Tyr Val Arg
175                               325                               330                               335
177 Ser Gly Lys Arg Leu Ala Ala Lys Gln Thr Arg Val Asp Ile Val Phe
178                               340                               345                               350
180 Lys Ala Gly Thr Phe Asn Phe Gly Ser Glu Gln Glu Ala Gln Glu Ala
181                               355                               360                               365
183 Val Leu Ser Ile Ile Ile Asp Pro Lys Gly Ala Ile Glu Leu Lys Leu
184                               370                               375                               380
186 Asn Ala Lys Ser Val Glu Asp Ala Phe Asn Thr Arg Thr Ile Asp Leu
187 385                               390                               395                               400
189 Gly Trp Thr Val Ser Asp Glu Asp Lys Lys Asn Thr Pro Glu Pro Tyr
190                               405                               410                               415
192 Glu Arg Met Ile His Asp Thr Met Asn Gly Asp Gly Ser Asn Phe Ala
193                               420                               425                               430
195 Asp Trp Asn Gly Val Ser Ile Ala Trp Lys Phe Val Asp Ala Ile Ser
196                               435                               440                               445
198 Ala Val Tyr Thr Ala Asp Lys Ala Pro Leu Glu Thr Tyr Lys Ser Gly
199                               450                               455                               460
201 Ser Met Gly Pro Glu Ala Ser Asp Lys Leu Leu Ala Ala Asn Gly Asp
202 465                               470                               475                               480
204 Ala Trp Val Phe Lys Gly
205                               485

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208 <210> SEQ ID NO: 7

209 <211> LENGTH: 39

210 <212> TYPE: DNA

211 <213> ORGANISM: Artificial Sequence *OK*

213 <220> FEATURE:

214 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer *OK*

216 <400> SEQUENCE: 7

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217 ataaggggta caccatgggtt tcagaaatca agacgtag          39
220 <210> SEQ ID NO: 8
221 <211> LENGTH: 30
222 <212> TYPE: DNA
223 <213> ORGANISM: Artificial Sequence
225 <220> FEATURE:
226 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer ✓
228 <400> SEQUENCE: 8
229 ttcccgggct ttaattaacc tttaaacacc          30
232 <210> SEQ ID NO: 9
233 <211> LENGTH: 30
234 <212> TYPE: DNA
235 <213> ORGANISM: Artificial Sequence
237 <220> FEATURE:
238 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer ✓
240 <400> SEQUENCE: 9
241 tggttgggta gctatggaaa aaccagaatc          30
244 <210> SEQ ID NO: 10
245 <211> LENGTH: 34
246 <212> TYPE: DNA
247 <213> ORGANISM: Artificial Sequence
249 <220> FEATURE:
250 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer ✓
252 <400> SEQUENCE: 10
253 taggatccag gtacgtctaa ttcttcaagg tatg          34
256 <210> SEQ ID NO: 11
257 <211> LENGTH: 32
258 <212> TYPE: DNA
259 <213> ORGANISM: Artificial Sequence
261 <220> FEATURE:
262 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer ✓
264 <400> SEQUENCE: 11
265 atggatccgc tgattcta aaacaatacct tc          32
268 <210> SEQ ID NO: 12
269 <211> LENGTH: 25
270 <212> TYPE: DNA
271 <213> ORGANISM: Artificial Sequence
273 <220> FEATURE:
274 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer ✓
276 <400> SEQUENCE: 12
277 aagcttgcat gcctgcaggt tcccg          25
280 <210> SEQ ID NO: 13
281 <211> LENGTH: 54
282 <212> TYPE: DNA
283 <213> ORGANISM: Artificial Sequence
285 <220> FEATURE:
286 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
287     oligonucleotide consisting of DNA coding for amino acids
288     of Sequence 2, and a partial restriction site of BamHI ✓

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289 consisting of 5' end of "gatcc" and 3' end of "g"
291 <400> SEQUENCE: 13
292 gatccgacat gtcgaggaag gcttttgtgt ttcccaaaga gtcggatact tccg 54
295 <210> SEQ ID NO: 14
296 <211> LENGTH: 54
297 <212> TYPE: DNA
298 <213> ORGANISM: Artificial Sequence
300 <220> FEATURE:
301 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic *OK*
302 oligonucleotide
304 <400> SEQUENCE: 14
305 gatccggaag tatccgactc tttgggaaac acaaaagcct tcctcgacat gtcg 54
308 <210> SEQ ID NO: 15
309 <211> LENGTH: 48
310 <212> TYPE: DNA
311 <213> ORGANISM: Artificial Sequence *OK*
313 <220> FEATURE:
314 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
315 oligonucleotide consisting of DNA coding for amino acids
316 of Sequence 3, and a partial restriction site of BamHI
317 consisting of 5' end of "gatcc" and 3' end of "g". *OK*
320 <400> SEQUENCE: 15
321 gatccgtgct gtcaccagat gagattaaca ccatttatct tggcgggg 48
324 <210> SEQ ID NO: 16
325 <211> LENGTH: 48
326 <212> TYPE: DNA
327 <213> ORGANISM: Artificial Sequence *OK*
329 <220> FEATURE:
330 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic *OK*
331 oligonucleotide
333 <400> SEQUENCE: 16
334 gatccccgc caagatagat ggtgttaatc tcatttggtg acagcacg 48
337 <210> SEQ ID NO: 17
338 <211> LENGTH: 42
339 <212> TYPE: DNA
340 <213> ORGANISM: Artificial Sequence *OK*
342 <220> FEATURE:
343 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
344 oligonucleotide consisting of DNA coding for amino acids
345 of Sequence 4, and a partial restriction site of BamHI
346 consisting of 5' end of "gatcc" and 3' end of "g" *OK*
349 <400> SEQUENCE: 17
350 gatccctgaa gaagggatac actgtggggg cagaagcaag cg 42
353 <210> SEQ ID NO: 18
354 <211> LENGTH: 42
355 <212> TYPE: DNA
356 <213> ORGANISM: Artificial Sequence
358 <220> FEATURE:
359 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic

check

VERIFICATION SUMMARY

DATE: 10/23/2001

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Input Set : A:\55970281.app

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